of interest are substantially free from other compounds when they are within preparations that are at least 60% by weight (dry weight) the compound of interest. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight the compound of interest. Purity can be measured by any appropriate standard method, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

Where a particular polypeptide or nucleic acid molecule is said to have a specific percent identity to a reference polypeptide or nucleic acid molecule of a defined length, the percent identity is relative to the reference polypeptide or nucleic acid molecule. Thus, a peptide that is 50% identical to a reference polypeptide that is 100 amino acids long can be a 50 amino acid polypeptide that is completely identical to a 50 amino acid long portion of the reference polypeptide. It might also be a 100 amino acid long polypeptide which is 50% identical to the reference polypeptide over its entire length. Of course, many other polypeptides will meet the same criteria. The same rule applies for nucleic acid molecules.

For polypeptides, the length of the reference polypeptide sequence will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids, 50 amino acids, or 100 amino acids. For nucleic acids, the length of the reference nucleic acid sequence will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably at least 100 nucleotides (*e.g.*, 150, 200, 250, or 300 nucleotides).

In the case of polypeptide sequences that are less than 100% identical to a reference sequence, the non-

identical positions are preferably, but not necessarily, conservative substitutions for the reference sequence. Conservative substitutions typically include substitutions within the following groups: glycine and alanine; valine, isoleucine, and leucine; aspartic acid and glutamic acid; asparagine and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine.

Sequence identity can be measured using sequence analysis software (*e.g.*, the Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705 with the default parameters as specified therein.

The BLAST programs, provided as a service by the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov), are very useful for making sequence comparisons. The programs are described in detail by Karlin *et al.*, (*Proc. Natl. Acad. Sci. USA* 87:2264-68, 1990 and 90:5873-7, 1993) and Altschul *et al.*, (*Nucl. Acids Res.* 25:3389-3402, 1997) and are available on the internet at: http://www.ncbi.nlm.nih.gov.

The invention also features a host cell that harbors an isolated nucleic acid molecule encoding GLUTX (either alone or in conjunction with a heterologous polypeptide, such as a detectable marker) or a nucleic acid vector that contains a sequence encoding GLUTX (again, with or without a heterologous polypeptide). The vector can be an expression vector, and the expression vector can include a regulatory element. An antibody that specifically binds a GLUTX polypeptide is also within the scope of the present invention and is useful, for example, to detect GLUTX in a biological sample or to alter the activity of GLUTX. For example, GLUTX can be detected in a biological sample by

contacting the sample with an antibody that specifically binds GLUTX under conditions that allow the formation of a GLUTX-antibody complex and detecting the complex, if present, as an indication of the presence of GLUTX in the sample. The use of an antibody in a treatment regime, where it can alter the activity of GLUTX, is discussed further below.

An antibody of the invention can be a monoclonal, polyclonal, or engineered antibody that specifically binds GLUTX (as described more fully below). An antibody that "specifically binds" to a particular antigen, for example, a GLUTX polypeptide of the invention, will not substantially recognize or bind to other molecules in a sample, *e.g.*, a biological sample, that includes GLUTX.

Given that an object of the present invention is to alter the expression or activity of GLUTX in vivo, a pharmaceutical composition containing, for example, an isolated nucleic acid molecule encoding GLUTX (or a fragment thereof), a nucleic acid molecule that is antisense to GLUTX (*i.e.*, that has a sequence that is the reverse and complement of a portion of the coding strand of a GLUTX gene), a GLUTX polypeptide, or an antibody, small molecule, or other compound that specifically binds a GLUTX polypeptide is also a feature of the invention.

The discovery and characterization of GLUTX and the polypeptide it encodes makes it possible to determine whether a given disorder is associated with aberrant expression of GLUTX (either at the transcriptional or translational level) or activity of GLUTX. For example, one can diagnose a patient as having a disorder associated with aberrant expression of GLUTX by measuring GLUTX expression in a biological sample obtained from the patient. An increase or decrease in GLUTX expression in the biological